

SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals s.a.

<120> Novel Compounds

<130> B45282

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 909

<212> DNA

<213> Dermatophagoides pteronyssinus

<220>

<221> CDS

<222> (1)...(906)

<400> 1

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg
195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc ggc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210> 2

<211> 302

<212> PRT

<213> Dermatophagoides pteronyssinus

<400> 2

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145 150 155 160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
195 200 205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
210 215 220

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225 230 235 240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

<210> 3

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C4R mutant of ProDer p 1

<400> 3

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145 150 155 160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
195 200 205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
210 215 220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225 230 235 240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

<210> 4

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C4R mutant of ProDer p 1

<400> 4

cg_g cg_g ag_c tc_c att aag acc tc_c gag gaa tac aag aaa gc_c tc_c aac 48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Ala Phe Asn
1 5 10 15

aag ag_c tat gc_c acc tc_c gag gac gag gag gc_c gc_c aag aac tc_c 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30

ct_g gaa ag_c gt_g aaa tac gt_g cag ag_c aac gg_c ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45

ct_g tc_c gac ct_g tct tt_a gac gag tc_c aag aac cg_g tc_c ct_g at_g ag_c 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60

gc_c gag gct tc_c gaa cac ctt aag acc cag ttt gat ctc aac gc_c gag 240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80

acc aac gc_c cgt agt at_c aac gg_c aat gc_c ccc gct gag att gat ct_g 288
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95

cg_c cag at_g agg acc gt_g act ccc at_c cg_c at_g caa gg_c gg_c tg_c ggg 336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110

tct tgt tgg gc_c tt_t tca gg_c gt_g gc_c gc_c aca gag tc_c gca tac ctc 384

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Gly Ile

210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210> 5

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C31R mutant of ProDer p 1

<400> 5

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
 85 90 95
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly
 100 105 110
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
 115 120 125
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
 130 135 140
 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
 145 150 155 160
 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
 165 170 175
 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
 180 185 190
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
 195 200 205
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
 210 215 220
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
 225 230 235 240
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
 245 250 255
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
 260 265 270
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
 275 280 285
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
 290 295 300

<210> 6

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C31R mutant of ProDer p 1

<400> 6

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Ala Ala Arg Lys Asn Phe
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc cgt ggg 336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly

100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Gly Ile

210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210> 7

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C65R mutant of ProDer p 1

<400> 7

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50	55	60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu		
65	70	75
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu		
85	90	95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly		
100	105	110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu		
115	120	125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp		
130	135	140
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile		
145	150	155
160		
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr		
165	170	175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly		
180	185	190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg		
195	200	205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Gly Ile		
210	215	220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln		
225	230	235
240		
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly		
245	250	255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp		
260	265	270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile		
275	280	285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu		
290	295	300

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C65R mutant of ProDer p 1

<400> 8

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Ala Ala Arg Lys Asn Phe
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

cgt gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290 295 300

taa 909

<210> 9

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C71R mutant of ProDer p 1

<400> 9

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140
Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile
145 150 155 160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
195 200 205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Gly Ile
210 215 220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225 230 235 240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

<210> 10

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C71R mutant of ProDer p 1

<400> 10

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384
Ser Cys Thr Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140

tgc gcc tcc caa cac gga cgt cat ggg gat acg att ccc aga ggt atc 480
Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile
145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg
195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gac aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290 295 300

taa 909

<210> 11

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C103R mutant of ProDer p 1

<400> 11

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1	5	10	15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe			
20	25	30	
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
35	40	45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	
Val Ala Arg Glu Gln Ser Arg Arg Arg Pro Asn Ala Gln Arg Phe Gly			
180	185	190	
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Ile Arg			
195	200	205	
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile			
210	215	220	
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln			
225	230	235	240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly			
245	250	255	
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp			
260	265	270	
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile			

275 280 285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

<210> 12
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(906)

<223> C103R mutant of ProDer p 1

<400> 12
cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Ala Ala Arg Lys Asn Phe
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Ala Ile Asn His
35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc cgt cgc cgt cct aac gca cag cgc ttc ggc 576

Val Ala Arg Glu Gln Ser Arg Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210

215

220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225

230

235

240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245

250

255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260

265

270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275

280

285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290

295

300

taa

909

<210> 13

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C117R mutant of ProDer p 1

<400> 13

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145 150 155 160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190
Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
195 200 205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
210 215 220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225 230 235 240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

<210> 14

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C117R mutant of ProDer p 1

<400> 14

cgg ccc agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Ala Ala Arg Lys Asn Phe
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tcc aat tat cgt cag atc tac ccc cct aat gcc aac aag atc agg 624
Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg
195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Gly Ile
210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210> 15

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 15

ttaagaccca gtttgtatctc aacgcggaga ccaacgcccgtatcaacggc aatgcccccg 60
ctgagattga tctgcgccag atgaggaccg tgactccat ccgcattgc 108

<210> 16

<211> 103

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 16

cggatggag tcacggtcct catctggcgc agatcaatct cagcgggggc attgccgttgc 60
atactacggg cgttgttctc cgcgttgaga tcgaaaactgg gtc 103

<210> 17

<211> 92

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 17

caaggcggcc gtgggtcttg ttggccctt tcagggcgtgg ccgcgcacaga gtcggcatac 60
ctcgcgtatc ggaatcagag cctggacactc gc 92

<210> 18

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 18

tcagcgaggt ccaggctctg attccgatac gcgaggatg ccgactctgt cgccggccacg 60
cctgaaaagg cccacaaga cccacggcccg ccttgcatg 99

<210> 19

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 19

tgagcaggag ctcgttgacc gtgcctccca acacggatgt catggggata cgattccag 60
aggtatcgaa tacatccagc ata 83

<210> 20

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20

ctggatgtat tcgataccctc tggaaatcgat atccccatg acatccgtgt tgggaggcac 60
ggtaaacgcg ctcctgc 77

<210> 21

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

actgacaggc ctgcggccgag ctccattaa 29

<210> 22

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

cagtacaccta ggtcttagact cgaggggat 29

<210> 23

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

ggctttcgaa caccctaaga cccag 25

<210> 24

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

gctccctagc tacgtatcgg taatagc

27

<210> 25

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

cctcgcgtat cggcaacaga gcctggacc

29

<210> 26

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

ggtccaggct ctgttgccga tacgcgagg

29